

OM protein - protein search, using sw model

Run on: December 6, 2005, 18:05:17 ; Search time 133.243 Seconds  
(without alignments)  
1490.508 Million cell updates/sec

Title: US-10-782-002-35  
Perfect score: 2505  
Sequence: 1 MMMKQYLQYLAAALPLVGLA.....DAQVWSNIRFGPIGSTYDF 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 18:09:07 ; Search time 26.1361 Seconds  
(without alignments)  
1663.984 Million cell updates/sec

Title: US-10-782-002-35  
Perfect score: 2505  
Sequence: 1 MMMKQYLQYLAAALPLVGLA.....DAQVWSNIRFGPIGSTYDF 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*

3: pir3:\*  
4: pir4:\*

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 18:06:47 ; Search time 157.841 Seconds  
(without alignments)  
2020.377 Million cell updates/sec

Title: US-10-782-002-35  
Perfect score: 2505  
Sequence: 1 MMMKQYLQYLAAALPLVGLA.....DAQVVWSNIRFGPIGSTYDF 452

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 18:05:17 ; Search time 126.757 Seconds  
(without alignments)  
1490.508 Million cell updates/sec

Title: US-10-782-002-35\_COPY\_23\_452  
Perfect score: 2398  
Sequence: 1 QRAGNETPENHPPLTWQRCT.....DAQVVWSNIRFGPIGSTYDF 430

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*

4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

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OM protein - protein search, using sw model

Run on: December 6, 2005, 18:09:07 ; Search time 24.8639 Seconds  
(without alignments)  
1663.984 Million cell updates/sec

Title: US-10-782-002-35\_COPY\_23\_452  
Perfect score: 2398  
Sequence: 1 QRAGNETPENHPPLTWQRCT.....DAQVWSNIRFGPIGSTYDF 430

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 18:06:47 ; Search time 150.159 Seconds  
(without alignments)  
2020.377 Million cell updates/sec

Title: US-10-782-002-35\_COPY\_23\_452  
Perfect score: 2398  
Sequence: 1 QRAGNETPENHPPLTWQRCT.....DAQVWSNIRFGPIGSTYDF 430

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*